



SEQUENCE LISTING

<110> Nohyaku Co., Ltd.

<120> NOVEL PROTOPORPHYRINOGEN OXIDASE TOLERANT TO PHOTBLEACHING HERBICIDE

<130> Q58140

<140> 09/508,418

<141> 2000-03-13

<150> JP 9-265084

<151> 1997-09-11

<160> 11

<170> PatentIn version 3.0

<210> 1

<211> 1874

<212> DNA

<213> Nicotiana tabacum

<220>

<221> exon

<222> (26)..(1672)

<220>

<221> misc_feature

<223> Strain name: Xanthi NC

<400> 1

```

agcgcgggtct acaagtcagg cagtc atg aca aca act ccc atc gcc aat cat      52
                               Met Thr Thr Thr Pro Ile Ala Asn His
                               1                               5

cct aat att ttc act cac cag tcg tcg tca tcg cca ttg gca ttc tta      100
Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu
10                               15                               20                               25

aac cgt acg agt ttc atc cct ttc tct tca atc tcc aag cgc aat agt      148
Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser
                               30                               35                               40

gtc aat tgc aat ggc tgg aga aca cga tgc tcc gtt gcc aaa gat tac      196
Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr
                               45                               50                               55

aca gtt cct tcc tca gcg gtc gac ggc gga ccc gcc gcg gag ctg gac      244
Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp
                               60                               65                               70

tgt gtt ata gtt gga gca gga att agt ggc ctc tgc att gcg cag gtg      292
Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val

```

75	80	85	
atg tcc gct aat tac ccc aat ttg atg gta acc gag gcg aga gat cgt			340
Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg			
90	95	100	105
gcc ggt ggc aac ata acg act gtg gaa aga gac ggc tat ttg tgg gaa			388
Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu			
	110	115	120
gaa ggt ccc aac agt ttc cag ccg tcc gat cct atg ttg act atg gca			436
Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala			
	125	130	135
gta gat tgt gga ttg aag gat gat ttg gtg ttg gga gat cct aat gcg			484
Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala			
	140	145	150
ccc cgt ttc gtt ttg tgg aag ggt aaa tta agg ccc gtc ccc tca aaa			532
Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys			
	155	160	165
ctc act gat ctt ccc ttt ttt gat ttg atg agc att cct ggc aag ttg			580
Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu			
170	175	180	185
aga gct ggt ttt ggt ccc att ggc ctc cgc cct tca cct cca ggt cat			628
Arg Ala Gly Phe Gly Pro Ile Gly Leu Arg Pro Ser Pro Pro Gly His			
	190	195	200
gag gaa tca gtt gag cag ttc gtg cgt cgt aat ctt ggt ggc gaa gtc			676
Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val			
	205	210	215
ttt gaa cgc ttg ata gaa cca ttt tgt tct ggt gtt tat gct ggt gat			724
Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp			
	220	225	230
ccc tca aaa ctg agt atg aaa gca gca ttt ggg aaa gtt tgg aag ttg			772
Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu			
	235	240	245
gaa gaa act ggt ggt agc att att gga gga acc ttt aaa gca ata aag			820
Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys			
250	255	260	265
gag aga tcc agt aca cct aaa gcg ccc cgc gat ccg cgt tta cct aaa			868
Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys			
	270	275	280
cca aaa gga cag aca gtt gga tca ttc agg aag ggt ctc aga atg ctg			916
Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu			
	285	290	295
ccg gat gca atc agt gca aga ttg gga agc aaa tta aaa cta tca tgg			964

Pro	Asp	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Ser	Lys	Leu	Lys	Leu	Ser	Trp		
		300					305					310					
aag	ctt	tct	agc	att	act	aag	tca	gaa	aaa	gga	gga	tat	cac	ttg	aca	1012	
Lys	Leu	Ser	Ser	Ile	Thr	Lys	Ser	Glu	Lys	Gly	Gly	Tyr	His	Leu	Thr		
	315					320				325							
tac	gag	aca	cca	gaa	gga	gta	gtt	tct	ctt	caa	agt	cga	agc	att	gtc	1060	
Tyr	Glu	Thr	Pro	Glu	Gly	Val	Val	Ser	Leu	Gln	Ser	Arg	Ser	Ile	Val		
330				335				340						345			
atg	act	gtg	cca	tcc	tat	gta	gca	agc	aac	ata	tta	cgt	cct	ctt	tcg	1108	
Met	Thr	Val	Pro	Ser	Tyr	Val	Ala	Ser	Asn	Ile	Leu	Arg	Pro	Leu	Ser		
			350					355						360			
gtt	gcc	gca	gca	gat	gca	ctt	tca	aat	ttc	tac	tat	ccc	cca	gtt	gga	1156	
Val	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Asn	Phe	Tyr	Tyr	Pro	Pro	Val	Gly		
		365					370					375					
gca	gtc	aca	att	tca	tat	cct	caa	gaa	gct	att	cgt	gat	gag	cgt	ctg	1204	
Ala	Val	Thr	Ile	Ser	Tyr	Pro	Gln	Glu	Ala	Ile	Arg	Asp	Glu	Arg	Leu		
		380				385					390						
gtt	gat	ggt	gaa	cta	aag	gga	ttt	ggg	cag	ttg	cat	cca	cgt	aca	cag	1252	
Val	Asp	Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His	Pro	Arg	Thr	Gln		
	395				400				405								
gga	gtg	gaa	aca	cta	gga	acg	ata	tat	agt	tca	tca	ctc	ttc	cct	aac	1300	
Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser	Leu	Phe	Pro	Asn		
410				415					420					425			
cgt	gcc	cca	aaa	ggt	cgg	gtg	cta	ctc	ttg	aac	tac	att	gga	gga	gca	1348	
Arg	Ala	Pro	Lys	Gly	Arg	Val	Leu	Leu	Leu	Asn	Tyr	Ile	Gly	Gly	Ala		
			430				435						440				
aaa	aat	cct	gaa	att	ttg	tct	aag	acg	gag	agc	caa	ctt	gtg	gaa	gta	1396	
Lys	Asn	Pro	Glu	Ile	Leu	Ser	Lys	Thr	Glu	Ser	Gln	Leu	Val	Glu	Val		
		445				450					455						
gtt	gat	cgt	gac	ctc	aga	aaa	atg	ctt	ata	aaa	ccc	aaa	gct	caa	gat	1444	
Val	Asp	Arg	Asp	Leu	Arg	Lys	Met	Leu	Ile	Lys	Pro	Lys	Ala	Gln	Asp		
		460				465					470						
cct	ctt	gtt	gtg	ggt	gtg	cga	gta	tgg	cca	caa	gct	atc	cca	cag	ttt	1492	
Pro	Leu	Val	Val	Gly	Val	Arg	Val	Trp	Pro	Gln	Ala	Ile	Pro	Gln	Phe		
	475				480					485							
ttg	gtt	ggt	cat	ctg	gat	acg	cta	agt	act	gca	aaa	gct	gct	atg	aat	1540	
Leu	Val	Gly	His	Leu	Asp	Thr	Leu	Ser	Thr	Ala	Lys	Ala	Ala	Met	Asn		
490				495				500						505			
gat	aat	ggg	ctt	gaa	ggg	ctg	ttt	ctt	ggg	ggt	aat	tat	gtg	tca	ggt	1588	
Asp	Asn	Gly	Leu	Glu	Gly	Leu	Phe	Leu	Gly	Gly	Asn	Tyr	Val	Ser	Gly		
			510					515					520				

Asp Leu Val Leu Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Lys
 145 150 155 160

Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr Asp Leu Pro Phe Phe
 165 170 175

Asp Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Phe Gly Pro Ile
 180 185 190

Gly Leu Arg Pro Ser Pro Pro Gly His Glu Glu Ser Val Glu Gln Phe
 195 200 205

Val Arg Arg Asn Leu Gly Gly Glu Val Phe Glu Arg Leu Ile Glu Pro
 210 215 220

Phe Cys Ser Gly Val Tyr Val Gly Asp Pro Ser Lys Leu Ser Met Lys
 225 230 235 240

Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Glu Thr Gly Gly Ser Ile
 245 250 255

Ile Gly Gly Thr Phe Lys Ala Ile Lys Glu Arg Ser Ser Thr Pro Lys
 260 265 270

Ala Pro Arg Asp Pro Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly
 275 280 285

Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Asp Ala Ile Ser Ala Arg
 290 295 300

Leu Gly Ser Lys Leu Lys Leu Ser Trp Lys Leu Ser Ser Ile Thr Lys
 305 310 315 320

Ser Glu Lys Gly Gly Tyr His Leu Thr Tyr Glu Thr Pro Glu Gly Val
 325 330 335

Val Ser Leu Gln Ser Arg Ser Ile Val Met Thr Val Pro Ser Tyr Val
 340 345 350

Ala Ser Asn Ile Leu Arg Pro Leu Ser Val Ala Ala Ala Asp Ala Leu
 355 360 365

Ser Asn Phe Tyr Tyr Pro Pro Val Gly Ala Val Thr Ile Ser Tyr Pro
 370 375 380

Gln Glu Ala Ile Arg Asp Glu Arg Leu Val Asp Gly Glu Leu Lys Gly
 385 390 395 400

Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val Glu Thr Leu Gly Thr
 405 410 415

Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Lys Gly Arg Val
 420 425 430

Leu Leu Leu Asn Tyr Ile Gly Gly Ala Lys Asn Pro Glu Ile Leu Ser
435 440 445

Lys Thr Glu Ser Gln Leu Val Glu Val Val Asp Arg Asp Leu Arg Lys
450 455 460

Met Leu Ile Lys Pro Lys Ala Gln Asp Pro Leu Val Val Gly Val Arg
465 470 475 480

Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Thr
485 490 495

Leu Ser Thr Ala Lys Ala Ala Met Asn Asp Asn Gly Leu Glu Gly Leu
500 505 510

Phe Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val
515 520 525

Glu Gly Ala Tyr Glu Val Ala Ser Glu Val Thr Gly Phe Leu Ser Arg
530 535 540

Tyr Ala Tyr Lys
545

<210> 3
<211> 1874
<212> DNA
<213> Nicotiana tabacum

<220>
<221> exon
<222> (26)..(1672)

<220>
<221> misc_feature
<223> Strain name: SR1

<400> 3
agcgcgggtct acaagtcagg cagtc atg aca aca act ccc atc gcc aat cat 52
Met Thr Thr Thr Pro Ile Ala Asn His
1 5

cct aat att ttc act cac cag tcg tcg tca tcg cca ttg gca ttc tta 100
Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu
10 15 20 25

aac cgt acg agt ttc atc cct ttc tct tca atc tcc aag cgc aat agt 148
Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser
30 35 40

gtc aat tgc aat ggc tgg aga aca cga tgc tcc gtt gcc aaa gat tac 196
Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr
45 50 55

aca gtt cct tcc tca gcg gtc gac ggc gga ccc gcc gcg gag ctg gac	244
Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp	
60 65 70	
tgt gtt ata gtt gga gca gga att agt ggc ctc tgc att gcg cag gtg	292
Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val	
75 80 85	
atg tcc gct aat tac ccc aat ttg atg gta acc gag gcg aga gat cgt	340
Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg	
90 95 100 105	
gcc ggt ggc aac ata acg act gtg gaa aga gac ggc tat ttg tgg gaa	388
Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu	
110 115 120	
gaa ggt ccc aac agt ttc cag ccg tcc gat cct atg ttg act atg gca	436
Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala	
125 130 135	
gta gat tgt gga ttg aag gat gat ttg gtg ttg gga gat cct aat gcg	484
Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala	
140 145 150	
ccc cgt ttc gtt ttg tgg aag ggt aaa tta agg ccc gtc ccc tca aaa	532
Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys	
155 160 165	
ctc act gat ctt ccc ttt ttt gat ttg atg agc att cct ggc aag ttg	580
Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu	
170 175 180 185	
aga gct ggt ttt ggt gcc att ggc ctc cgc cct tca cct cca ggt cat	628
Arg Ala Gly Phe Gly Ala Ile Gly Leu Arg Pro Ser Pro Pro Gly His	
190 195 200	
gag gaa tca gtt gag cag ttc gtg cgt cgt aat ctt ggt ggc gaa gtc	676
Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val	
205 210 215	
ttt gaa cgc ttg ata gaa cca ttt tgt tct ggt gtt tat gtt ggt gat	724
Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Val Gly Asp	
220 225 230	
ccc tca aaa ctg agt atg aaa gca gca ttt ggg aaa gtt tgg aag ttg	772
Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu	
235 240 245	
gaa gaa act ggt ggt agc att att gga gga acc ttt aaa gca ata aag	820
Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys	
250 255 260 265	
gag aga tcc agt aca cct aaa gcg ccc cgc gat ccg cgt tta cct aaa	868
Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys	
270 275 280	

cca aaa gga cag aca gtt gga tca ttc agg aag ggt ctc aga atg ctg 916
Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu
285 290 295

ccg gat gca atc agt gca aga ttg gga agc aaa tta aaa cta tca tgg 964
Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp
300 305 310

aag ctt tct agc att act aag tca gaa aaa gga gga tat cac ttg aca 1012
Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr
315 320 325

tac gag aca cca gaa gga gta gtt tct ctt caa agt cga agc att gtc 1060
Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val
330 335 340 345

atg act gtg cca tcc tat gta gca agc aac ata tta cgt cct ctt tcg 1108
Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser
350 355 360

gtt gcc gca gca gat gca ctt tca aat ttc tac tat ccc cca gtt gga 1156
Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly
365 370 375

gca gtc aca att tca tat cct caa gaa gct att cgt gat gag cgt ctg 1204
Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu
380 385 390

gtt gat ggt gaa cta aag gga ttt ggg cag ttg cat cca cgt aca cag 1252
Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
395 400 405

gga gtg gaa aca cta gga acg ata tat agt tca tca ctc ttc cct aac 1300
Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn
410 415 420 425

cgt gcc cca aaa ggt cgg gtg cta ctc ttg aac tac att gga gga gca 1348
Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala
430 435 440

aaa aat cct gaa att ttg tct aag acg gag agc caa ctt gtg gaa gta 1396
Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val
445 450 455

gtt gat cgt gac ctc aga aaa atg ctt ata aaa ccc aaa gct caa gat 1444
Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp
460 465 470

cct ctt gtt gtg ggt gtg cga gta tgg cca caa gct atc cca cag ttt 1492
Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe
475 480 485

ttg gtt ggt cat ctg gat acg cta agt act gca aaa gct gct atg aat 1540
Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn

490	495	500	505	
gat aat ggg ctt gaa ggg ctg ttt ctt ggg ggt aat tat gtg tca ggt				1588
Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly				
	510	515	520	
gta gca ttg ggg agg tgt gtt gaa ggt gct tat gaa gtt gca tcc gag				1636
Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu				
	525	530	535	
gta aca gga ttt ctg tct cgg tat gca tac aaa tga aacctgtgtt				1682
Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys				
	540	545		
gggggtagtc caaaccttgt tagtagtacg atcatgcctt gggaaaattg gcatgtgcct				1742
aaaagttttg ctcatagag ttatttttagc cttggtaaatt gatttgtact tgatatcagt				1802
cgttttcttt gagataaaat gttcctgttc aggaaatata atgtatatca attttaaaca				1862
aaaaaaaaaa aa				1874
<210> 4				
<211> 23				
<212> DNA				
<213> artificial sequence				
<220>				
<223> lambda-gt22A forward primer				
<400> 4				
attggtggcg acgactcctg gag				23
<210> 5				
<211> 24				
<212> DNA				
<213> artificial sequence				
<220>				
<223> lambda-gt22A reverse primer				
<400> 5				
ccagaccaac tgtaaatggt agcg				24
<210> 6				
<211> 24				
<212> DNA				
<213> artificial sequence				
<220>				
<223> forward primer				

<400> 6
 gcggtctaca agtcaggcag tcat 24

<210> 7
 <211> 31
 <212> DNA
 <213> artificial sequence

<220>
 <223> reverse primer

<400> 7
 catgcccaatt ttccaaggc atgatcgtac t 31

<210> 8
 <211> 20
 <212> DNA
 <213> artificial sequence

<220>
 <223> mutagenic primer

<400> 8
 ggtgtttatg ttggtgatcc 20

<210> 9
 <211> 27
 <212> DNA
 <213> artificial sequence

<220>
 <223> CaMV 35S promoter forward primer

<400> 9
 cacagatggt tagagaggct tacgcac 27

<210> 10
 <211> 27
 <212> DNA
 <213> artificial sequence

<220>
 <223> Nos terminator reverse primer

<400> 10
 tcatcgcaag accggcaaca ggattca 27

<210> 11
 <211> 537
 <212> PRT

<213> Arabidopsis thaliana

<400> 11

Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser Leu Leu Pro Ser
1 5 10 15
Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys Pro Leu Arg Leu
20 25 30
Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser Ser Lys Ile Glu
35 40 45
Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val Ile Val Gly Gly
50 55 60
Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala Thr Lys His Pro
65 70 75 80
Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys Asp Arg Val Gly
85 90 95
Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu Trp Glu Glu Gly
100 105 110
Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Val Val Asp
115 120 125
Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Thr Ala Pro Arg
130 135 140
Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr
145 150 155 160
Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala
165 170 175
Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu
180 185 190
Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu
195 200 205
Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser
210 215 220
Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Gln
225 230 235 240
Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg
245 250 255
Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln
260 265 270

Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu
 275 280 285

Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu
 290 295 300

Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu
 305 310 315 320

Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr
 325 330 335

Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser
 340 345 350

Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
 355 360 365

Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
 370 375 380

Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val
 385 390 395 400

Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala
 405 410 415

Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn
 420 425 430

Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp
 435 440 445

Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu
 450 455 460

Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val
 465 470 475 480

Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser
 485 490 495

Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala
 500 505 510

Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala Ile Glu Val Asn
 515 520 525

Asn Phe Met Ser Arg Tyr Ala Tyr Lys
 530 535